FIG. 1

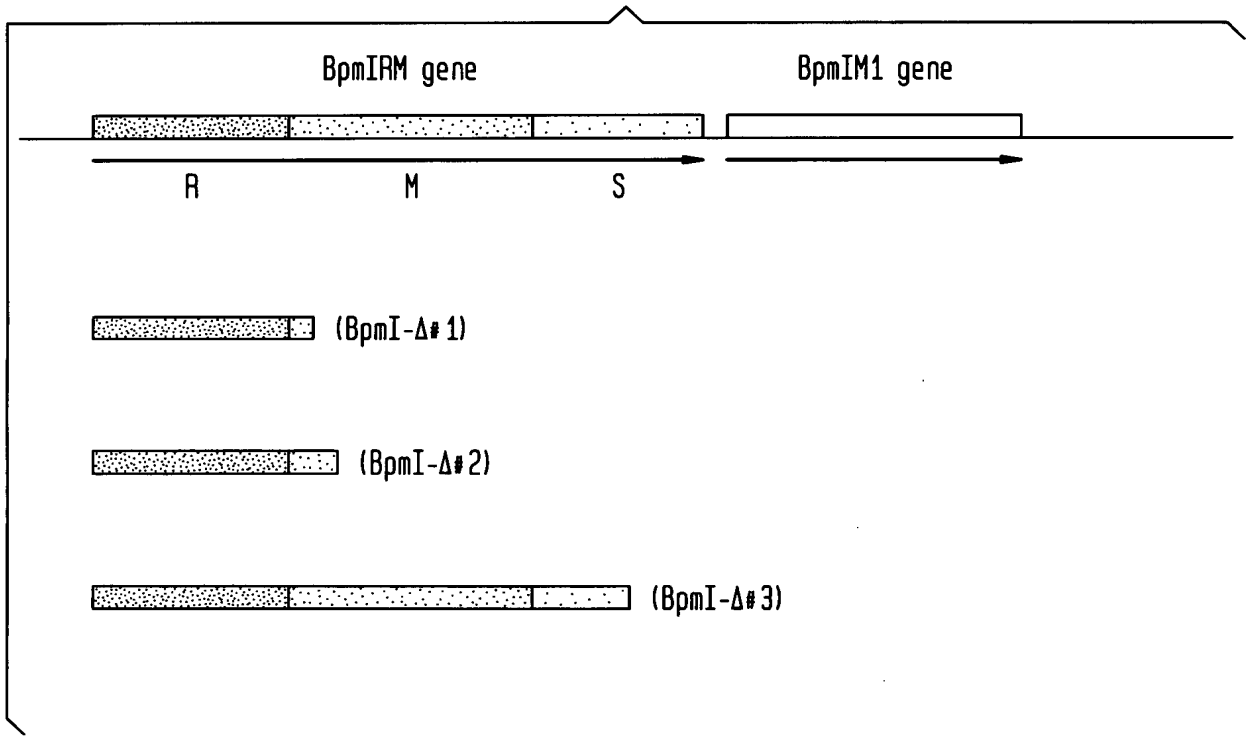
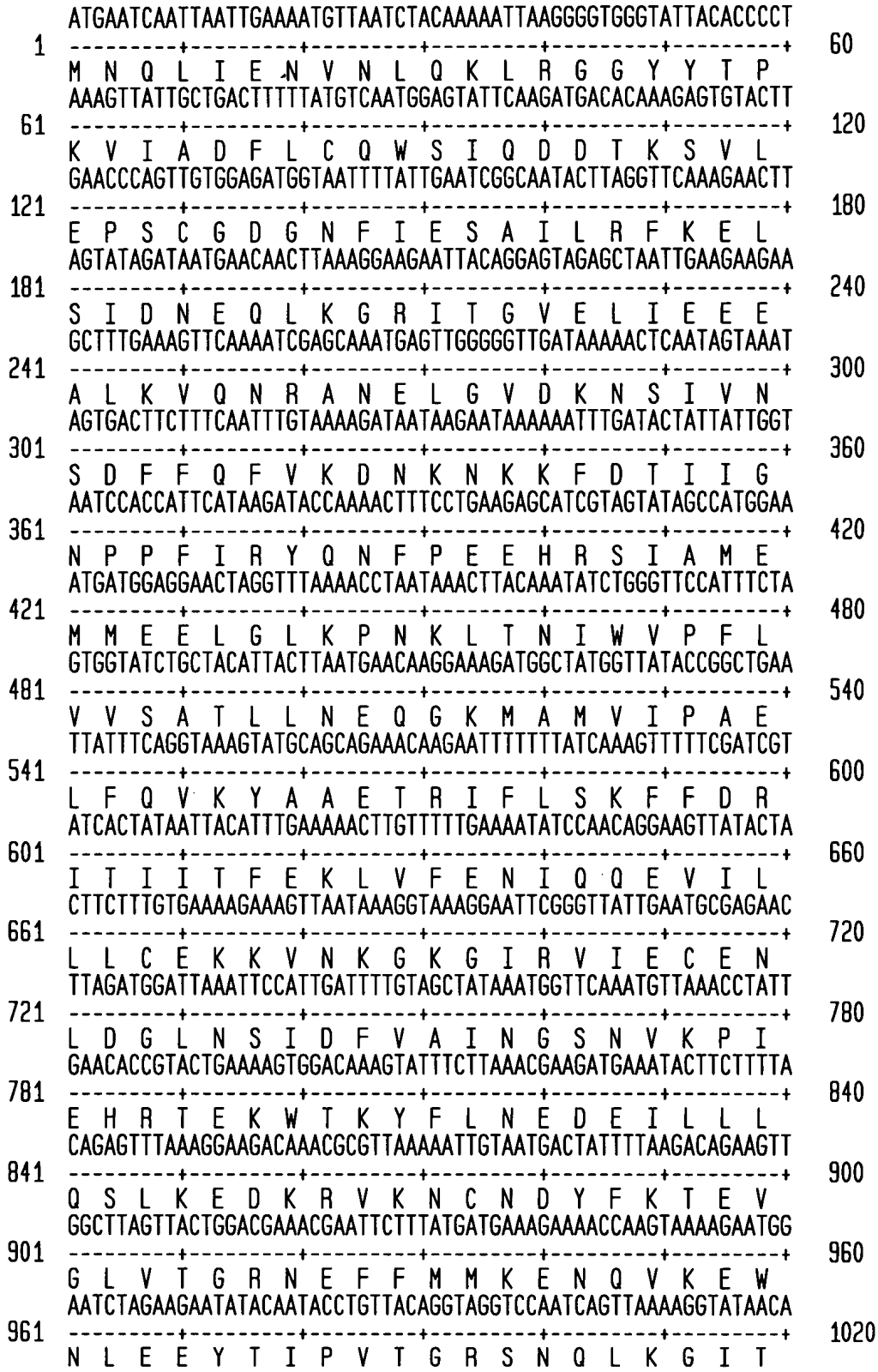


FIG. 2A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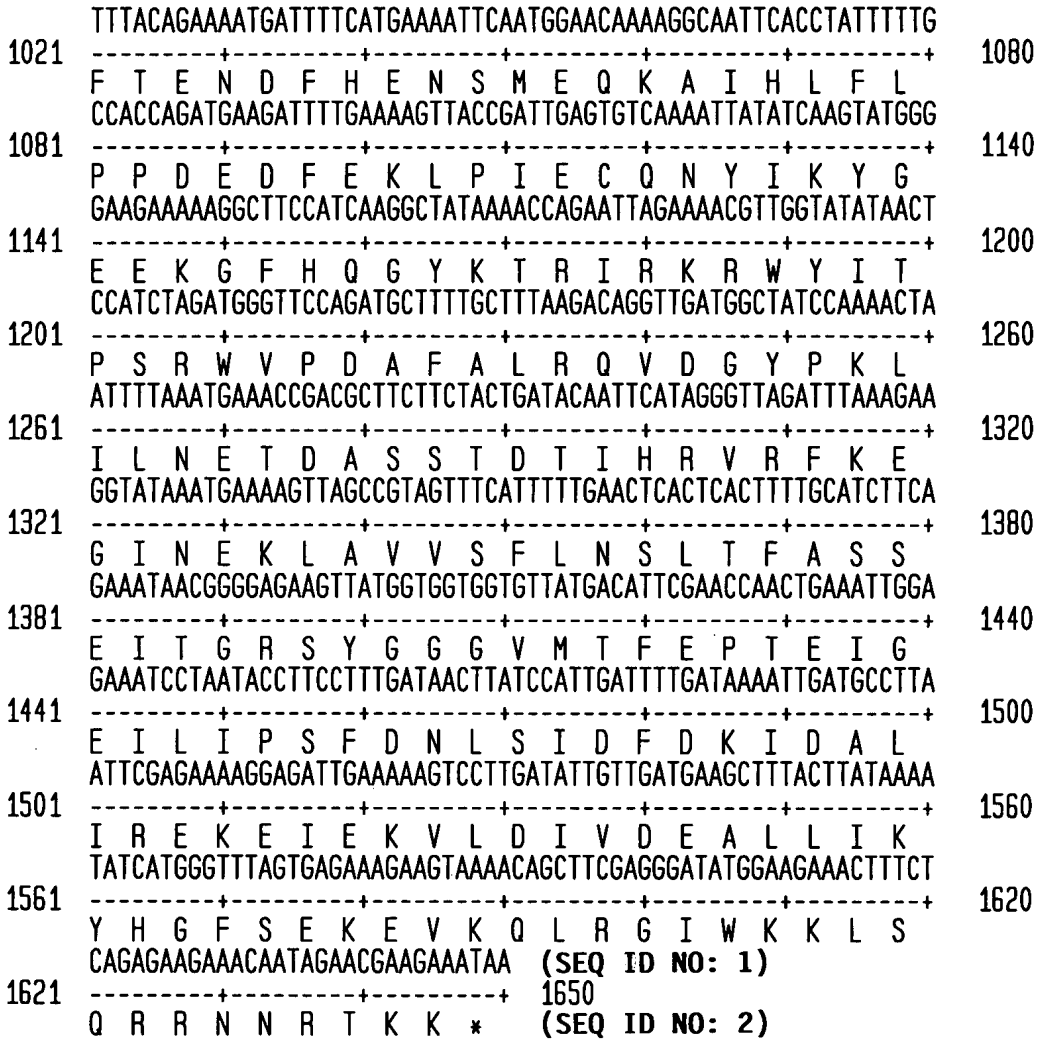
1
60
M N Q L I E N V N L Q K L R G G Y Y T P
AAAGTTATTGCTGACTTTTTATGTCAATGGAGTATTCAAGATGACACAAAGAGTGTACTT
61
120
K V I A D F L C Q W S I Q D D T K S V L
GAACCCAGTTGTGGAGATGGTAATTTTATTGAATCGGCAATACTTAGGTTCAAAGAACTT
121
180
E P S C G D G N F I E S A I L R F K E L
AGTATAGATAATGAACAACTTAAAGGAAGAATTACAGGAGTAGAGCTAATTGAAGAAGAA
181
240
S I D N E Q L K G R I T G V E L I E E E
GCTTTGAAAGTTCAAAATCGAGCAAATGAGTTGGGGGTTGATAAAAACTCAATAGTAAAT
241
300
A L K V Q N R A N E L G V D K N S I V N
AGTGACTTCTTTCAATTTGTAAAAGATAATAAGAATAAAAAATTTGATACTATTATTGGT
301
360
S D F F Q F V K D N K N K K F D T I I G
AATCCACCATTCATAAGATACCAAAACTTTCCTGAAGAGCATCGTAGTATAGCCATGGAA
361
420
N P P F I R Y Q N F P E E H R S I A M E
ATGATGGAGGAACTAGGTTTAAAACCTAATAAACTTACAAATATCTGGGTTCCATTTCTA
421
480
M M E E L G L K P N K L T N I W V P F L
GTGGTATCTGCTACATTACTTAATGAACAAGGAAAGATGGCTATGGTTATACCGGCTGAA
481
540
V V S A T L L N E Q G K M A M V I P A E
TTATTTCAGGTAAAGTATGCAGCAGAAACAAGAATTTTTTTATCAAAGTTTTTCGATCGT
541
600
L F Q V K Y A A E T R I F L S K F F D R
ATCACTATAATTACATTTGAAAAACTTGTTTTTGAAAATATCCAACAGGAAGTTATACTA
601
660
I T I I T F E K L V F E N I Q Q E V I L
CTTCTTTGTGAAAAGAAAGTTAATAAAGGTAAAGGAATTCGGGTTATTGAATGCGAGAAC
661
720
L L C E K K V N K G K G I R V I E C E N
TTAGATGGATTAAATTCCATTGATTTTGTAGCTATAAATGGTTCAAATGTTAAACCTATT
721
780
L D G L N S I D F V A I N G S N V K P I
GAACACCGTACTGAAAAGTGGACAAAGTATTTCTTAAACGAAGATGAAATACTTCTTTTA
781
840
E H R T E K W T K Y F L N E D E I L L L
CAGAGTTTAAAGGAAGACAAACGCGTTAAAAATTGTAATGACTATTTTAAGACAGAAGTT
841
900
Q S L K E D K R V K N C N D Y F K T E V
GGCTTAGTTACTGGACGAAACGAATTCTTTATGATGAAAGAAAACCAAGTAAAAGAATGG
901
960
G L V T G R N E F F M M K E N Q V K E W
AATCTAGAAGAATATACAATACCTGTTACAGGTAGGTCCAATCAGTTAAAAGGTATAACA
961
1020
N L E E Y T I P V T G R S N Q L K G I T

FIG. 2B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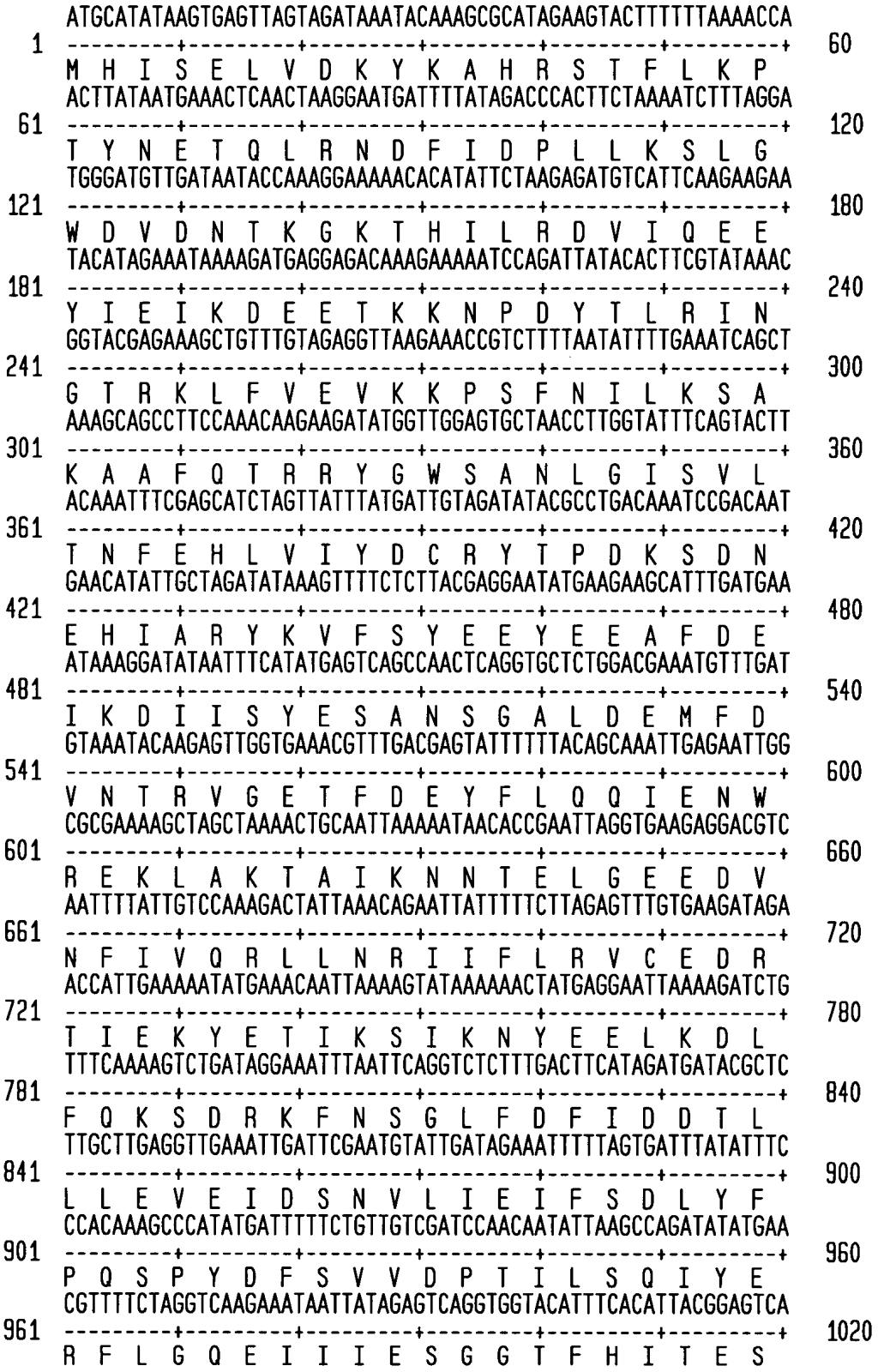
1021 1080
F T E N D F H E N S M E Q K A I H L F L
CCACCAGATGAAGATTTTGAAAAGTTACCGATTGAGTGTCAAAATTATATCAAGTATGGG
1081 1140
P P D E D F E K L P I E C Q N Y I K Y G
GAAGAAAAAGGCTTCCATCAAGGCTATAAAACCAGAATTAGAAAACGTTGGTATATAACT
1141 1200
E E K G F H Q G Y K T R I R K R W Y I T
CCATCTAGATGGGTTCCAGATGCTTTTGCTTTAAGACAGGTTGATGGCTATCCAAAACTA
1201 1260
P S R W V P D A F A L R Q V D G Y P K L
ATTTTAAATGAAACCGACGCTTCTTCTACTGATACAATTCATAGGGTTAGATTTAAAGAA
1261 1320
I L N E T D A S S T D T I H R V R F K E
GGTATAAATGAAAAGTTAGCCGTAGTTTCATTTTTGAACTCACTCACTTTTGCATCTTCA
1321 1380
G I N E K L A V V S F L N S L T F A S S
GAAATAACGGGGAGAAGTTATGGTGGTGGTGTTATGACATTCGAACCAACTGAAATTGGA
1381 1440
E I T G R S Y G G G V M T F E P T E I G
GAAATCCTAATACCTTCCTTTGATAACTTATCCATTGATTTTGATAAAATTGATGCCTTA
1441 1500
E I L I P S F D N L S I D F D K I D A L
ATTCGAGAAAAGGAGATTGAAAAAGTCCTTGATATTGTTGATGAAGCTTTACTTATAAAA
1501 1560
I R E K E I E K V L D I V D E A L L I K
TATCATGGGTTTAGTGAGAAAGAAGTAAAACAGCTTCGAGGGATATGGAAGAAACTTTCT
1561 1620
Y H G F S E K E V K Q L R G I W K K L S
CAGAGAAGAAACAATAGAACGAAGAAATAA (SEQ ID NO: 1)
1621 1650
Q R R N N R T K K * (SEQ ID NO: 2)

FIG. 3A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1 60
M H I S E L V D K Y K A H R S T F L K P
ACTTATAATGAAACTCAACTAAGGAATGATTTTATAGACCCACTTCTAAAATCTTTAGGA
61 120
T Y N E T Q L R N D F I D P L L K S L G
TGGGATGTTGATAATACCAAAGGAAAAACACATATTCTAAGAGATGTCATTCAAGAAGAA
121 180
W D V D N T K G K T H I L R D V I Q E E
TACATAGAAATAAAAGATGAGGAGACAAAGAAAAATCCAGATTATACACTTCGTATAAAC
181 240
Y I E I K D E E T K K N P D Y T L R I N
GGTACGAGAAAGCTGTTTGTAGAGGTTAAGAAACCGTCTTTTAATATTTTGAAATCAGCT
241 300
G T R K L F V E V K K P S F N I L K S A
AAAGCAGCCTTCCAAACAAGAAGATATGGTTGGAGTGCTAACCTTGGTATTTCAGTACTT
301 360
K A A F Q T R R Y G W S A N L G I S V L
ACAAATTTCGAGCATCTAGTTATTTATGATTGTAGATATACGCCTGACAAATCCGACAAT
361 420
T N F E H L V I Y D C R Y T P D K S D N
GAACATATTGCTAGATATAAAGTTTTCTCTTACGAGGAATATGAAGAAGCATTTGATGAA
421 480
E H I A R Y K V F S Y E E Y E E A F D E
ATAAAGGATATAATTTCATATGAGTCAGCCAACTCAGGTGCTCTGGACGAAATGTTTGAT
481 540
I K D I I S Y E S A N S G A L D E M F D
GTAAATACAAGAGTTGGTGAAACGTTTGACGAGTATTTTTTACAGCAAATTGAGAATTGG
541 600
V N T R V G E T F D E Y F L Q Q I E N W
CGCGAAAAGCTAGCTAAAACTGCAATTAAAAATAACACCGAATTAGGTGAAGAGGACGTC
601 660
R E K L A K T A I K N N T E L G E E D V
AATTTTATTGTCCAAAGACTATTAAACAGAATTATTTTTCTTAGAGTTTGTGAAGATAGA
661 720
N F I V Q R L L N R I I F L R V C E D R
ACCATTGAAAAATATGAAACAATTAAAAGTATAAAAAACTATGAGGAATTAAAAGATCTG
721 780
T I E K Y E T I K S I K N Y E E L K D L
TTTCAAAAGTCTGATAGGAAATTTAATTCAGGTCTCTTTGACTTCATAGATGATACGCTC
781 840
F Q K S D R K F N S G L F D F I D D T L
TTGCTTGAGGTTGAAATTGATTCGAATGTATTGATAGAAATTTTTAGTGATTTATATTTC
841 900
L L E V E I D S N V L I E I F S D L Y F
CCACAAAGCCCATATGATTTTTCTGTTGTCGATCCAACAATATTAAGCCAGATATATGAA
901 960
P Q S P Y D F S V V D P T I L S Q I Y E
CGTTTTCTAGGTCAAGAAATAATTATAGAGTCAGGTGGTACATTTCACATTACGGAGTCA
961 1020
R F L G Q E I I I E S G G T F H I T E S

FIG. 3B

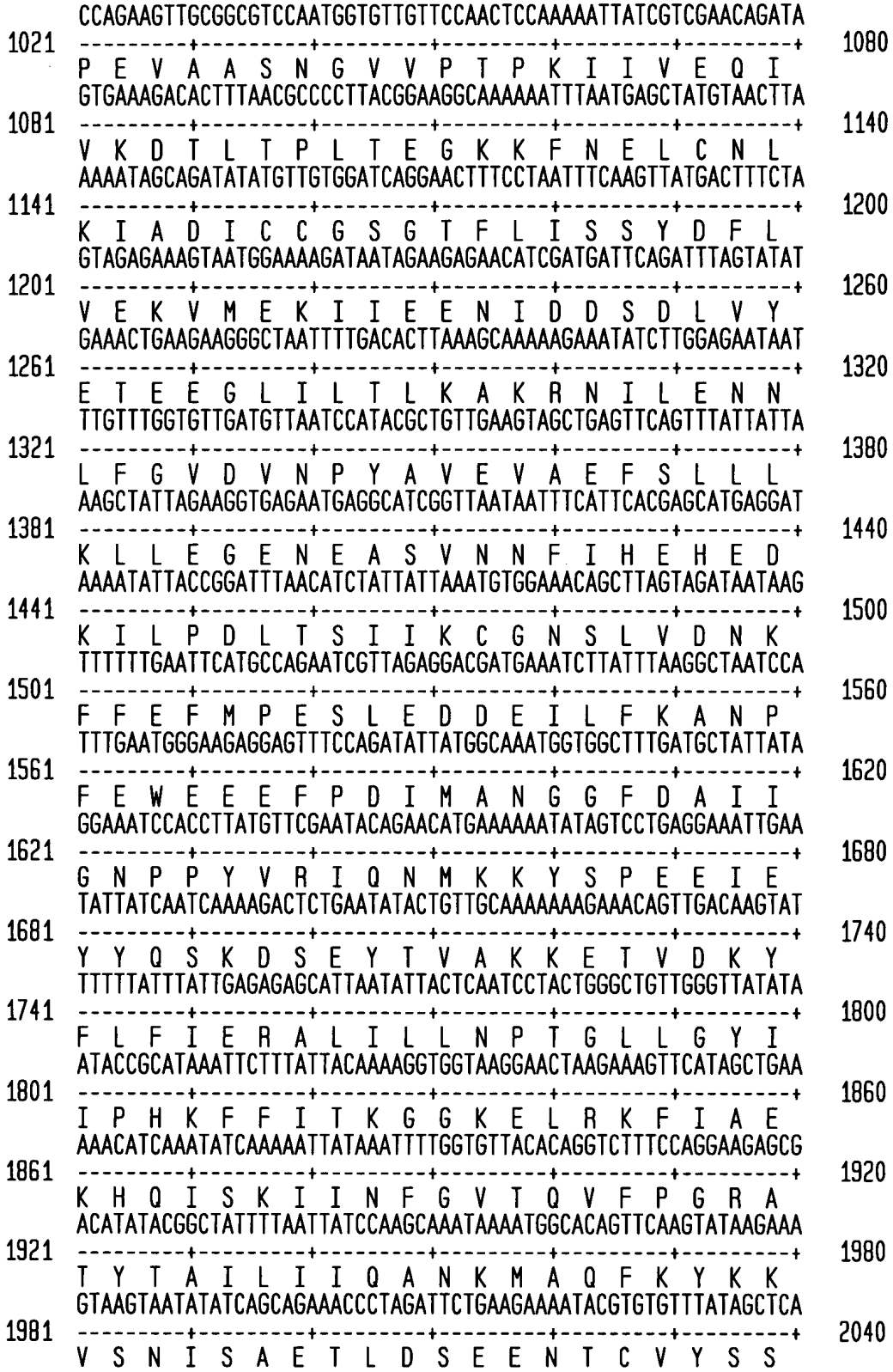
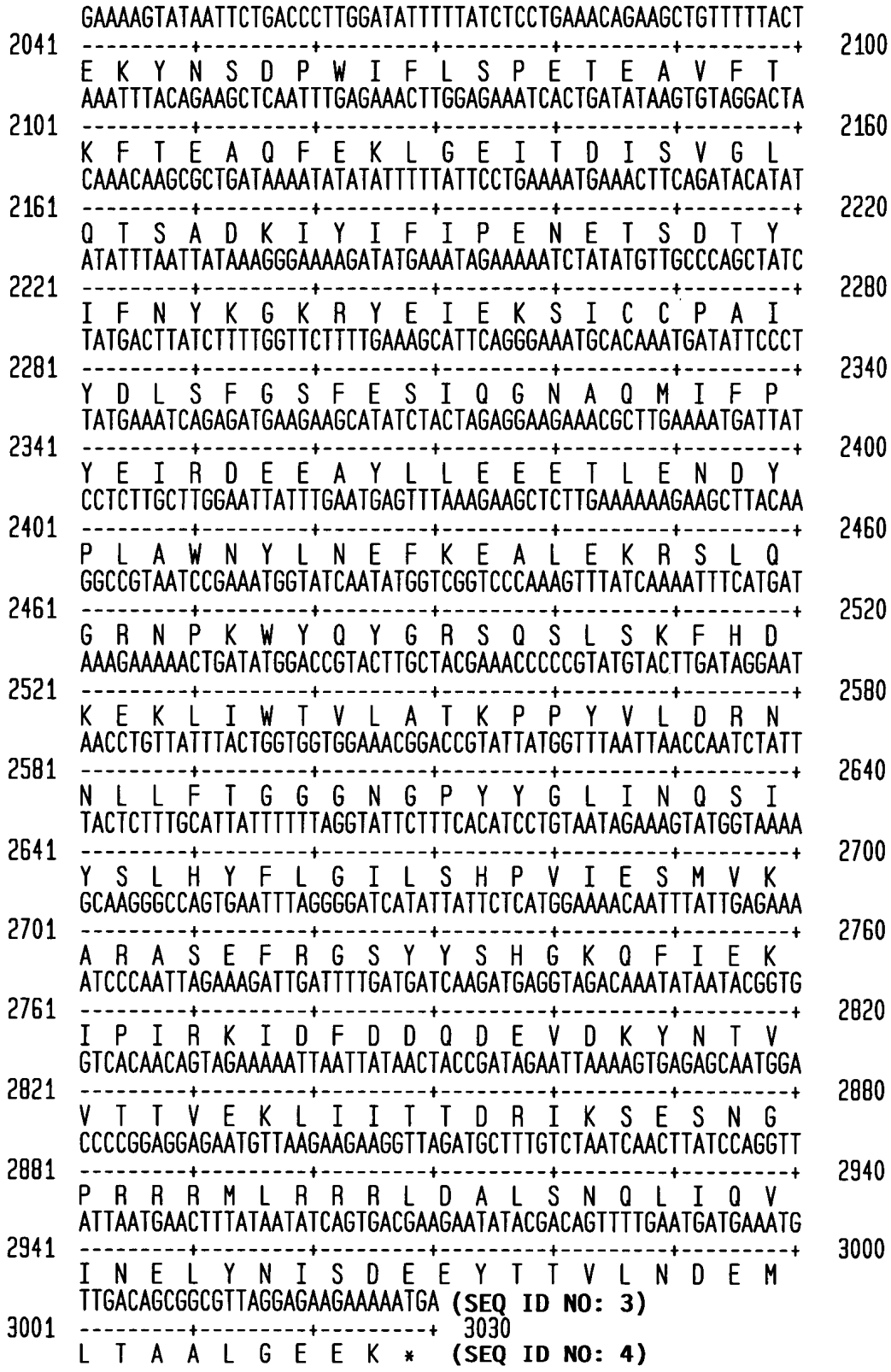

CCAGAAGTTGCGGCGTCCAATGGTGTTGTTCCAACTCCAAAAATTATCGTCGAACAGATA
1021 1080
P E V A A S N G V V P T P K I I V E Q I
GTGAAAGACACTTTAACGCCCCTTACGGAAGGCAAAAAATTTAATGAGCTATGTAACTTA
1081 1140
V K D T L T P L T E G K K F N E L C N L
AAAATAGCAGATATATGTTGTGGATCAGGAACTTTCCTAATTTCAAGTTATGACTTTCTA
1141 1200
K I A D I C C G S G T F L I S S Y D F L
GTAGAGAAAGTAATGGAAAAGATAATAGAAGAGAACATCGATGATTCAGATTTAGTATAT
1201 1260
V E K V M E K I I E E N I D D S D L V Y
GAAACTGAAGAAGGGCTAATTTTGACACTTAAAGCAAAAAGAAATATCTTGGAGAATAAT
1261 1320
E T E E G L I L T L K A K R N I L E N N
TTGTTTGGTGTTGATGTTAATCCATACGCTGTTGAAGTAGCTGAGTTCAGTTTATTATTA
1321 1380
L F G V D V N P Y A V E V A E F S L L L
AAGCTATTAGAAGGTGAGAATGAGGCATCGGTTAATAATTTCATTCACGAGCATGAGGAT
1381 1440
K L L E G E N E A S V N N F I H E H E D
AAAATATTACCGGATTTAACATCTATTATTAAATGTGGAAACAGCTTAGTAGATAATAAG
1441 1500
K I L P D L T S I I K C G N S L V D N K
TTTTTTGAATTCATGCCAGAATCGTTAGAGGACGATGAAATCTTATTTAAGGCTAATCCA
1501 1560
F F E F M P E S L E D D E I L F K A N P
TTTGAATGGGAAGAGGAGTTTCCAGATATTATGGCAAATGGTGGCTTTGATGCTATTATA
1561 1620
F E W E E E F P D I M A N G G F D A I I
GGAAATCCACCTTATGTTCGAATACAGAACATGAAAAAATATAGTCCTGAGGAAATTGAA
1621 1680
G N P P Y V R I Q N M K K Y S P E E I E
TATTATCAATCAAAAGACTCTGAATATACTGTTGCAAAAAAAGAAACAGTTGACAAGTAT
1681 1740
Y Y Q S K D S E Y T V A K K E T V D K Y
TTTTTATTTATTGAGAGAGCATTAATATTACTCAATCCTACTGGGCTGTTGGGTTATATA
1741 1800
F L F I E R A L I L L N P T G L L G Y I
ATACCGCATAAATTCTTTATTACAAAAGGTGGTAAGGAACTAAGAAAGTTCATAGCTGAA
1801 1860
I P H K F F I T K G G K E L R K F I A E
AAACATCAAATATCAAAAATTATAAATTTTGGTGTTACACAGGTCTTTCCAGGAAGAGCG
1861 1920
K H Q I S K I I N F G V T Q V F P G R A
ACATATACGGCTATTTTAATTATCCAAGCAAATAAAATGGCACAGTTCAAGTATAAGAAA
1921 1980
T Y T A I L I I Q A N K M A Q F K Y K K
GTAAGTAATATATCAGCAGAAACCCTAGATTCTGAAGAAAATACGTGTGTTTATAGCTCA
1981 2040
V S N I S A E T L D S E E N T C V Y S S

FIG. 3C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2041 2100
E K Y N S D P W I F L S P E T E A V F T
AAATTTACAGAAGCTCAATTTGAGAAACTTGGAGAAATCACTGATATAAGTGTAGGACTA
2101 2160
K F T E A Q F E K L G E I T D I S V G L
CAAACAAGCGCTGATAAAATATATATTTTTATTCCTGAAAATGAAACTTCAGATACATAT
2161 2220
Q T S A D K I Y I F I P E N E T S D T Y
ATATTTAATTATAAAGGGAAAAGATATGAAATAGAAAAATCTATATGTTGCCCAGCTATC
2221 2280
I F N Y K G K R Y E I E K S I C C P A I
TATGACTTATCTTTTGGTTCTTTTGAAAGCATTCAGGGAAATGCACAAATGATATTCCCT
2281 2340
Y D L S F G S F E S I Q G N A Q M I F P
TATGAAATCAGAGATGAAGAAGCATATCTACTAGAGGAAGAAACGCTTGAAAATGATTAT
2341 2400
Y E I R D E E A Y L L E E E T L E N D Y
CCTCTTGCTTGGAATTATTTGAATGAGTTTAAAGAAGCTCTTGAAAAAAGAAGCTTACAA
2401 2460
P L A W N Y L N E F K E A L E K R S L Q
GGCCGTAATCCGAAATGGTATCAATATGGTCGGTCCCAAAGTTTATCAAAATTTCATGAT
2461 2520
G R N P K W Y Q Y G R S Q S L S K F H D
AAAGAAAAACTGATATGGACCGTACTTGCTACGAAACCCCCGTATGTACTTGATAGGAAT
2521 2580
K E K L I W T V L A T K P P Y V L D R N
AACCTGTTATTTACTGGTGGTGGAAACGGACCGTATTATGGTTTAATTAACCAATCTATT
2581 2640
N L L F T G G G N G P Y Y G L I N Q S I
TACTCTTTGCATTATTTTTTAGGTATTCTTTCACATCCTGTAATAGAAAGTATGGTAAAA
2641 2700
Y S L H Y F L G I L S H P V I E S M V K
GCAAGGGCCAGTGAATTTAGGGGATCATATTATTCTCATGGAAAACAATTTATTGAGAAA
2701 2760
A R A S E F R G S Y Y S H G K Q F I E K
ATCCCAATTAGAAAGATTGATTTTGATGATCAAGATGAGGTAGACAAATATAATACGGTG
2761 2820
I P I R K I D F D D Q D E V D K Y N T V
GTCACAACAGTAGAAAAATTAATTATAACTACCGATAGAATTAAAAGTGAGAGCAATGGA
2821 2880
V T T V E K L I I T T D R I K S E S N G
CCCCGGAGGAGAATGTTAAGAAGAAGGTTAGATGCTTTGTCTAATCAACTTATCCAGGTT
2881 2940
P R R R M L R R R L D A L S N Q L I Q V
ATTAATGAACTTTATAATATCAGTGACGAAGAATATACGACAGTTTTGAATGATGAAATG
2941 3000
I N E L Y N I S D E E Y T T V L N D E M
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3001 3030
L T A A L G E E K * (SEQ ID NO: 4)

FIG. 4

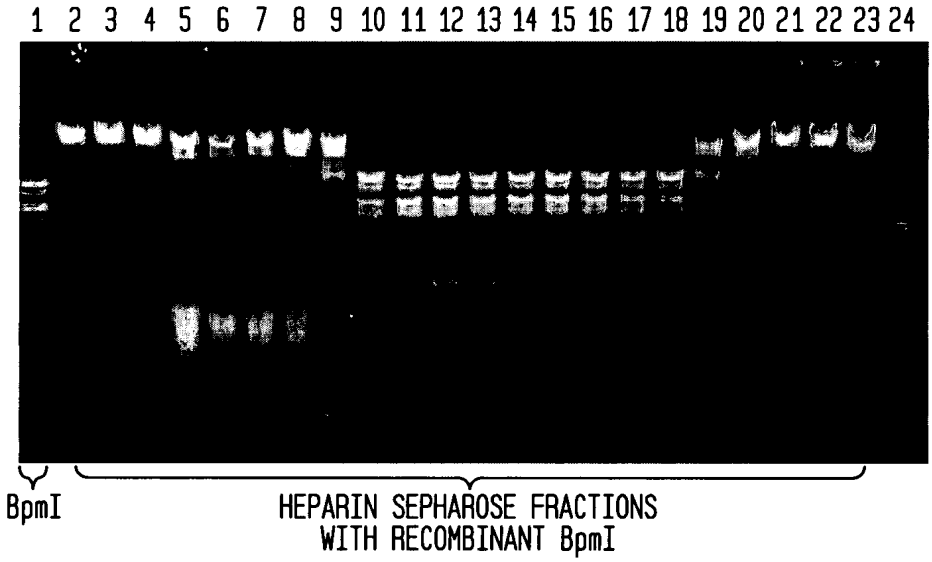


FIG. 5

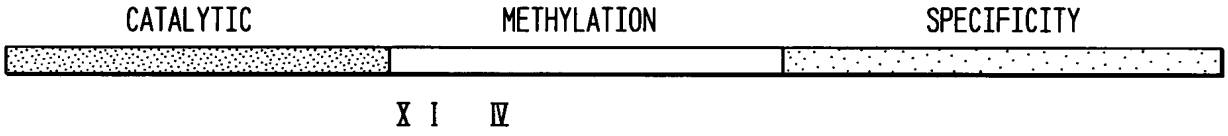


FIG. 6

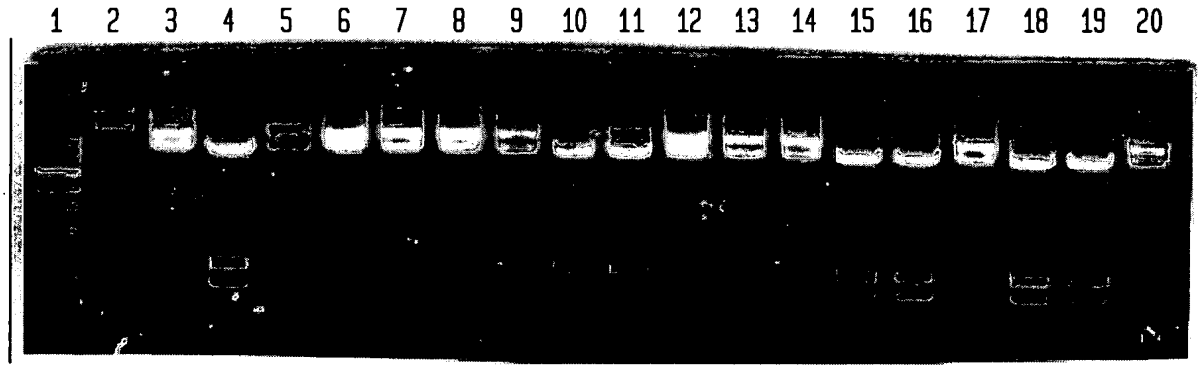


FIG. 7

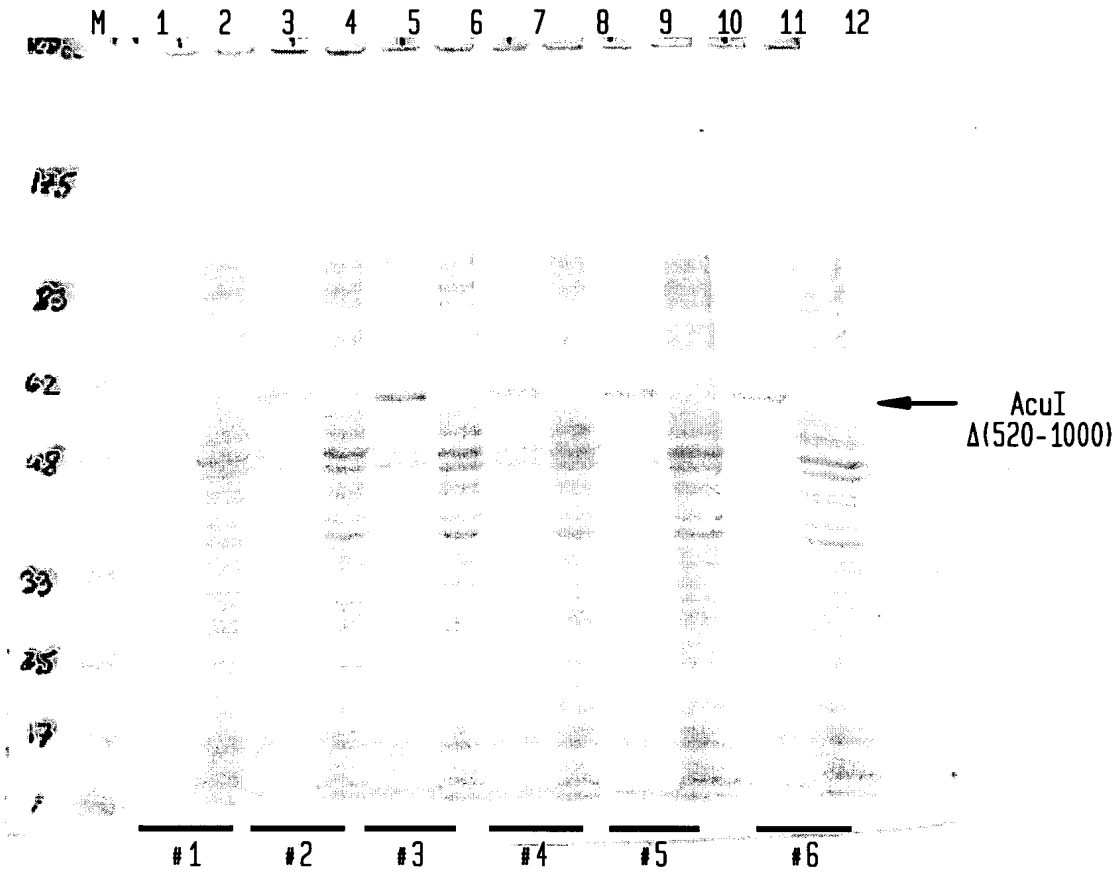

M
1
2
3
4
5
6
7
8
9
10
11
12
KDa
175
83
62
48
33
25
17
7
AcuI
Δ(520-1000)
#1
#2
#3
#4
#5
#6

FIG. 8

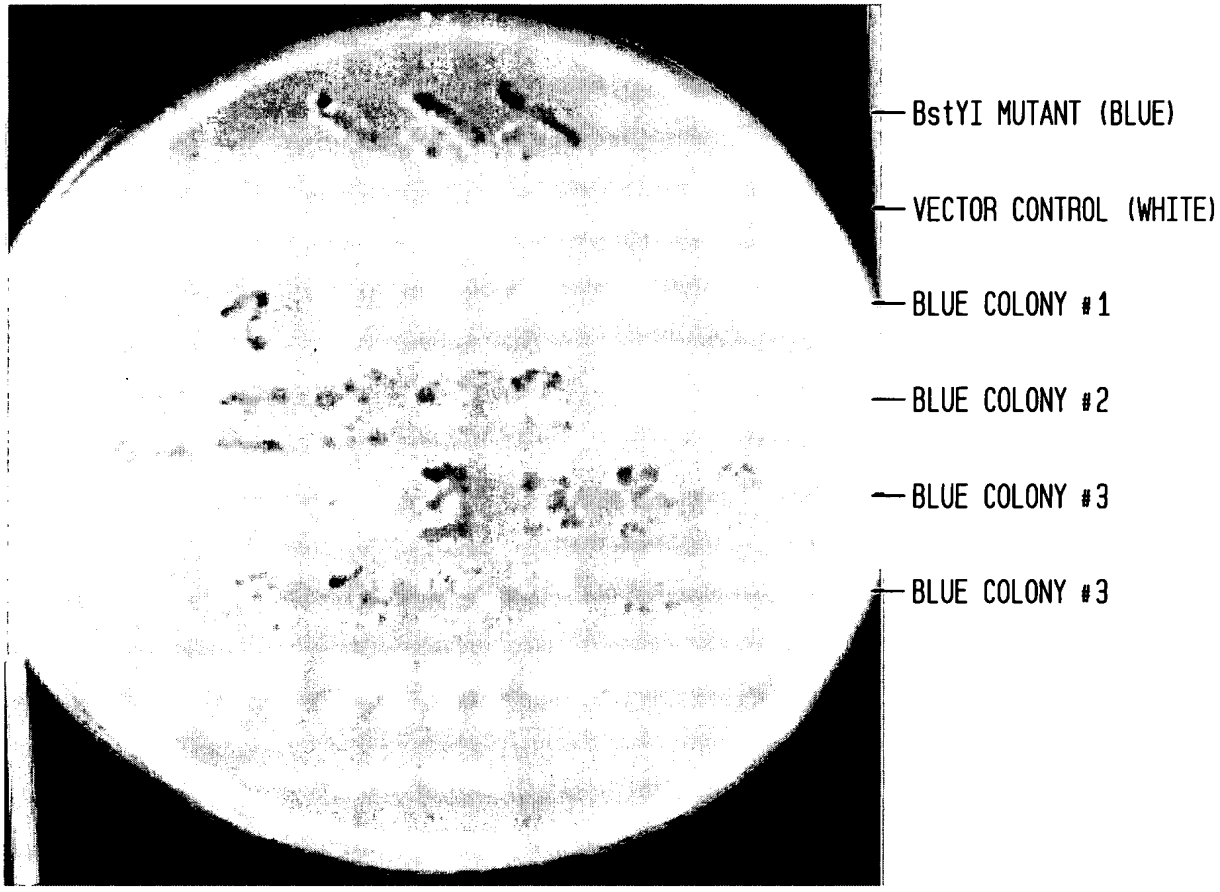
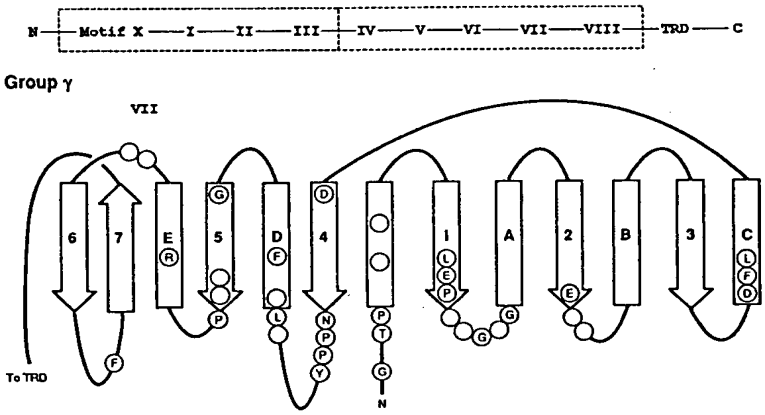
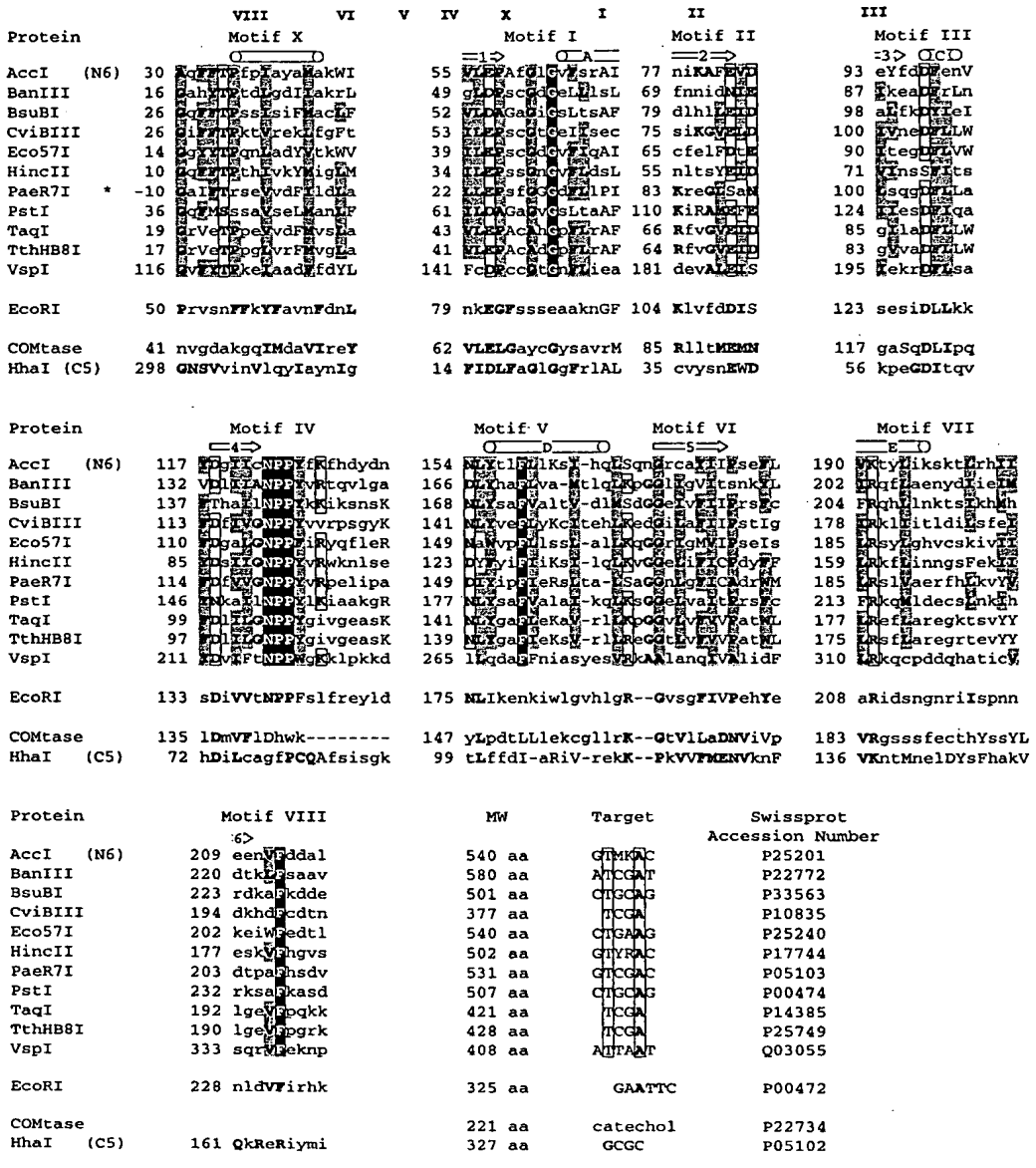

BstYI MUTANT (BLUE)
VECTOR CONTROL (WHITE)
BLUE COLONY #1
BLUE COLONY #2
BLUE COLONY #3
BLUE COLONY #3

FIG. 9


N
Motif X
I
II
III
IV
V
VI
VII
VIII
TRD
C
Group γ
To TRD


Protein
Motif X
Motif I
Motif II
Motif III
Motif IV
Motif V
Motif VI
Motif VII
Motif VIII
MW
Target
Swissprot Accession Number
AccI (N6)
BanIII
BsuBI
CviBIII
Eco57I
HincII
PaeR7I
PstI
TaqI
TthHB8I
VspI
EcoRI
COMtase
HhaI (C5)
540 aa
580 aa
501 aa
377 aa
540 aa
502 aa
531 aa
507 aa
421 aa
428 aa
408 aa
325 aa
221 aa
327 aa
GTMKAC
ATCGAT
CTGCAG
TCGA
CTCGAG
GTYRAC
GTCGAC
CTGCAG
TCGA
TCGA
AATTAAT
GAATTC
catechol
GCGC
P25201
P22772
P33563
P10835
P25240
P17744
P05103
P00474
P14385
P25749
Q03055
P00472
P22734
P05102